FIGURE 1A.1

```
ATG AAG CCG TAC TTC TGC CGT GTC TTT GTC TTC TGC TTC CTA ATC          45
M   K   P   Y   F   C   R   V   F   V   F   C   F   L   I
                5                   10                  15

AGA CTT TTA ACA GGA GAA ATC AAT GGC TCG GCC GAT CAT AGG ATG          90
R   L   L   T   G  *E   I   N   G   S   A   D   H   R   M
                20                  25                  30

TTT TCA TTT CAC AAT GGA GGT GTA CAG ATT TCT TGT AAA TAC CCT         135
F   S   F   H   N   G   G   V   Q   I   S   C   K   Y   P
                35                  40                  45

GAG ACT GTC CAG CAG TTA AAA ATG CGA TTG TTC AGA GAG AGA GAA         180
E   T   V   Q   Q   L   K   M   R   L   F   R   E   R   E
                50                  55                  60

GTC CTC TGC GAA CTC ACC AAG ACC AAG GGA AGC GGA AAT GCG GTG         225
V   L   C   E   L   T   K   T   K   G   S   G   N   A   V
                65                  70                  75

TCC ATC AAG AAT CCA ATG CTC TGT CTA TAT CAT CTG TCA AAC AAC         270
S   I   K   N   P   M   L   C   L   Y   H   L   S   N   N
                80                  85                  90

AGC GTC TCT TTT TTC CTA AAC AAC CCA GAC AGC TCC CAG GGA AGC         315
S   V   S   F   F   L   N   N   P   D   S   S   Q   G   S
                95                  100                 105

TAT TAC TTC TGC AGC CTG TCC ATT TTT GAC CCA CCT CCT TTT CAA         360
Y   Y   F   C   S   L   S   I   F   D   P   P   P   F   Q
                110                 115                 120

GAA AGG AAC CTT AGT GGA GGA TAT TTG CAT ATT TAT GAA TCC CAG         405
E   R   N   L   S   G   G   Y   L   H   I   Y   E   S   Q
                125                 130                 135

CTC TGC TGC CAG CTG AAG CTC TGG CTA CCC GTA GGG TGT GCA GCT         450
L   C   C   Q   L   K   L   W   L   P   V   G   C   A   A
                140                 145                 150

TTC GTT GTG GTA CTC CTT TTT GGA TGC ATA CTT ATC ATC TGG TTT         495
F   V   V   V   L   L   F   G   C   I   L   I   I   W   F
                155                 160                 165

TCA AAA AAG AAA TAC GGA TCC AGT GTG CAT GAC CCT AAT AGT GAA         540
S   K   K   K   Y   G   S   S   V   H   D   P   N   S   E
                170                 175                 180
```

FIGURE 1A.2

```
TAC ATG TTC ATG GCG GCA GTC AAC ACA AAC AAA AAG TCT AGA CTT          585
Y   M   F   M   A   A   V   N   T   N   K   K   S   R   L
                185                 190                 195

GCA GGT GTG ACC TCA                                                 600

A   G   V   T   S
                200
```

FIGURE 1B

```
mCRP1       MKPYFCRVFV FCFLIRLL-- -----TGEIN GS----ADHR MFSFHNGGVQ      39
mCD28       MT-------- ----LRLLFL ALNFFSVQVT ENKILVKQSP LLVVDSNEVS      38
Consensus   M......... .....RLL.. .......... .......... .........V.

mCRP1       ISCKYPETV- -QQLKMRLFR --EREV-LCE LTKTKGSGNA VSIKNPMLCL      84
mCD28       LSCRYSYNLL AKEFRASLYK GVNSDVEVCV GNGNFTYQPQ FRSNAEFNCD      88
Consensus   .SC.Y..... .......L.. .....V..C. .......... .........C.

mCRP1       YHLSNNSVSF FLNNPDSSQG SYYFCSLSIF DPPPFQERNL SGGYL-HIYE     133
mCD28       GDFDNETVTF RLWNLHVNHT DIYFCKIEFM YPPPYLDNER SNGTIIHIKE     138
Consensus   ....N..V.F .L.N...... ..YFC..... .PPP...... S.G...HI.E

mCRP1       SQLC---CQL KL-W-LPVGC AA-FVVVLLF GCIL-IIWFS KKKY----GS     172
mCD28       KHLCHTQSSP KLFWALVVVA GVLFCYGLLV TVALCVIWTN SRRNRLLQVT     188
Consensus   ..LC...... KL.W.L.V.. ...F...LL. ...L..IW.. ..........

mCRP1       SVH-DPNSEY MFMAAVNTNK KSR-LAGVTS                          200
mCD28       TMNMTPRRPG LTRKPYQPYA PARDFAAYRP                          218
Consensus   .....P.... .......... ..R..A.... ...
```

FIGURE 2A.1

```
ATG CAG CTA AAG TGT CCC TGT TTT GTG TCC TTG GGA ACC AGG CAG          45
M   Q   L   K   C   P   C   F   V   S   L   G   T   R   Q
                5                   10                  15

CCT GTT TGG AAG AAG CTC CAT GTT TCT AGC GGG TTC TTT TCT GGT          90
P   V   W   K   K   L   H   V   S   S   G   F   F   S   G
                20                  25                  30

CTT GGT CTG TTC TTG CTG CTG TTG AGC AGC CTC TGT GCT GCC TCT         135
L   G   L   F   L   L   L   L   S   S   L   C   A   A   S
                35                  40                  45

GCA GAG ACT GAA GTC GGT GCA ATG GTG GGC AGC AAT GTG GTG CTC         180
A  *E   T   E   V   G   A   M   V   G   S   N   V   V   L
                50                  55                  60

AGC TGC ATT GAC CCC CAC AGA CGC CAT TTC AAC TTG AGT GGT CTG         225
S   C   I   D   P   H   R   R   H   F   N   L   S   G   L
                65                  70                  75

TAT GTC TAT TGG CAA ATC GAA AAC CCA GAA GTT TCG GTG ACT TAC         270
Y   V   Y   W   Q   I   E   N   P   E   V   S   V   T   Y
                80                  85                  90

TAC CTG CCT TAC AAG TCT CCA GGG ATC AAT GTG GAC AGT TCC TAC         315
Y   L   P   Y   K   S   P   G   I   N   V   D   S   S   Y
                95                  100                 105

AAG AAC AGG GGC CAT CTG TCC CTG GAC TCC ATG AAG CAG GGT AAC         360
K   N   R   G   H   L   S   L   D   S   M   K   Q   G   N
                110                 115                 120

TTC TCT CTG TAC CTG AAG AAT GTC ACC CCT CAG GAT ACC CAG GAG         405
F   S   L   Y   L   K   N   V   T   P   Q   D   T   Q   E
                125                 130                 135

TTC ACA TGC CGG GTA TTT ATG AAT ACA GCC ACA GAG TTA GTC AAG         450
F   T   C   R   V   F   M   N   T   A   T   E   L   V   K
                140                 145                 150

ATC TTG GAA GAG GTG GTC AGG CTG CGT GTG GCA GCA AAC TTC AGT         495
I   L   E   E   V   V   R   L   R   V   A   A   N   F   S
                155                 160                 165

ACA CCT GTC ATC AGC ACC TCT GAT AGC TCC AAC CCG GGC CAG GAA         540
T   P   V   I   S   T   S   D   S   S   N   P   G   Q   E
                170                 175                 180
```

FIGURE 2A.2

```
CGT ACC TAC ACC TGC ATG TCC AAG AAT GGC TAC CCA GAG CCC AAC          585
R   T   Y   T   C   M   S   K   N   G   Y   P   E   P   N
                185                 190                 195

CTG TAT TGG ATC AAC ACA ACG GAC AAT AGC CTA ATA GAC ACG GCT          630
L   Y   W   I   N   T   T   D   N   S   L   I   D   T   A
                200                 205                 210

CTG CAG AAT AAC ACT GTC TAC TTG AAC AAG TTG GGC CTG TAT GAT          675
L   Q   N   N   T   V   Y   L   N   K   L   G   L   Y   D
                215                 220                 225

GTA ATC AGC ACA TTA AGG CTC CCT TGG ACA TCT CGT GGG GAT GTT          720
V   I   S   T   L   R   L   P   W   T   S   R   G   D   V
                230                 235                 240

CTG TGC TGC GTA GAG AAT GTG GCT CTC CAC CAG AAC ATC ACT AGC          765
L   C   C   V   E   N   V   A   L   H   Q   N   I   T   S
                245                 250                 255

ATT AGC CAG GCA GAA AGT TTC ACT GGA AAT AAC ACA AAG AAC CCA          810
I   S   Q   A   E   S   F   T   G   N   N   T   K   N   P
                260                 265                 270

CAG GAA ACC CAC AAT AAT GAG TTA AAA GTC CTT GTC CCC GTC CTT          855
Q   E   T   H   N   N   E   L   K   V   L   V   P   V   L
                275                 280                 285

GCT GTA CTG GCG GCA GCG GCA TTC GTT TCC TTC ATC ATA TAC AGA          900
A   V   L   A   A   A   A   F   V   S   F   I   I   Y   R
                290                 295                 300

CGC ACG CGT CCC CAC CGA AGC TAT ACA GGA CCC AAG ACT GTA CAG          945
R   T   R   P   H   R   S   Y   T   G   P   K   T   V   Q
                305                 310                 315

CTT GAA CTT ACA GAC CAC GCC                                          966

L   E   L   T   D   H   A
                320     322
```

FIGURE 2B

```
mB7RP1          MQLKCPCFVS LGTRQPVWKK LHVSSGFFSG LGLFLLLLS- SLCAASAETE   49
mCD80           MA--CNC--Q LMQDTPL--- LKFPCPRLI- L-LFVLLIRL SQVSSDVDEQ   41
Consensus       M...C.C... L....P.... L......... L.LF.LL... S.........

mB7RP1          VGAMVGSNVV LSCIDPHRRH FNLSGLYVYW QIENPEVSVT YYLPYKSPGI   99
mCD80           LSKSVKDKVL LPC-RYNSPH EDESEDRIYW QKHDKVV--- --LSVIAGKL   85
Consensus       ....V...V. L.C......H ...S....YW Q.....V... ..L.......

mB7RP1          NVDSSYKNRG HLSLDSMKQG NFSLYLKNVT PQDTQEFTCR VFMNTATELV  149
mCD80           KVWPEYKNR- --TL--YDNT TYSLIILGLV LSDRGTYSCV VQKKERGTYE  130
Consensus       .V...YKNR. ...L...... ..SL...... ..D.....C. V.........

mB7RP1          KILEEVVRLR VAANFSTPVI STSDSSNPGQ ERTYTCMSKN GYPEPNLYWI  199
mCD80           VKHLALVKLS IKADFSTPNI TESGNPSADT KRI-TCFASG GFPKPRFSWL  179
Consensus       ......V.L. ..A.FSTP.I ..S....... .R..TC.... G.P.P...W.


mB7RP1          -NTTDNSLID TALQNNTVYL NKLGLYDVIS TLRLPWTSRG DVLCCVENVA  248
mCD80           ENGRELPGIN TTISQDPESE LYTISSQLDF NTTRNHTIKC LIKYGDAHVS  229
Consensus       .N......I. T......... .......... ......T... ........V.

mB7RP1          LHQNITSISQ AESFTGNNTK NPQETHNNEL KVLVPVLAVL A-AAAFVSFI  297
mCD80           EDFTWEKPPE DPPDSKNTLV LFGAGFGAVI TVVVIVVIIK CFCKHRSCFR  279
Consensus       .......... ......N... .......... .V.V.V.... ........F.

mB7RP1          IYRRTR-PHR SYT-GPKTVQ LELTDHA                           322
mCD80           RNEASRETNN SLTFGPEEAL AEQTVFL                           306
Consensus       .....R.... S.T.GP.... .E.T...
```

FIGURE 3A.1


```
ATG CGG CTG GGC AGT CCT GGA CTG CTC TTC CTG CTC TTC AGC AGC          45
M   R   L   G   S   P   G   L   L   F   L   L   F   S   S
                5                   10                  15

CTT CGA GCT GAT ACT CAG GAG AAG GAA GTC AGA GCG ATG GTA GGC          90
L   R   A  *D  *T  *Q  *E   K  *E   V   R   A  *M   V   G
                20                  25                  30

AGC GAC GTG GAG CTC AGC TGC GCT TGC CCT GAA GGA AGC CGT TTT         135
S   D   V   E   L   S   C   A   C   P   E   G   S   R   F
                35                  40                  45

GAT TTA AAT GAT GTT TAC GTA TAT TGG CAA ACC AGT GAG TCG AAA         180
D   L   N   D   V   Y   V   Y   W   Q   T   S   E   S   K
                50                  55                  60

ACC GTG GTG ACC TAC CAC ATC CCA CAG AAC AGC TCC TTG GAA AAC         225
T   V   V   T   Y   H   I   P   Q   N   S   S   L   E   N
                65                  70                  75

GTG GAC AGC CGC TAC CGG AAC CGA GCC CTG ATG TCA CCG GCC GGC         270
V   D   S   R   Y   R   N   R   A   L   M   S   P   A   G
                80                  85                  90

ATG CTG CGG GGC GAC TTC TCC CTG CGC TTG TTC AAC GTC ACC CCC         315
M   L   R   G   D   F   S   L   R   L   F   N   V   T   P
                95                  100                 105

CAG GAC GAG CAG AAG TTT CAC TGC CTG GTG TTG AGC CAA TCC CTG         360
Q   D   E   Q   K   F   H   C   L   V   L   S   Q   S   L
                110                 115                 120

GGA TTC CAG GAG GTT TTG AGC GTT GAG GTT ACA CTG CAT GTG GCA         405
G   F   Q   E   V   L   S   V   E   V   T   L   H   V   A
                125                 130                 135

GCA AAC TTC AGC GTG CCC GTC GTC AGC GCC CCC CAC AGC CCC TCC         450
A   N   F   S   V   P   V   V   S   A   P   H   S   P   S
                140                 145                 150

CAG GAT GAG CTC ACC TTC ACG TGT ACA TCC ATA AAC GGC TAC CCC         495
Q   D   E   L   T   F   T   C   T   S   I   N   G   Y   P
                155                 160                 165

AGG CCC AAC GTG TAC TGG ATC AAT AAG ACG GAC AAC AGC CTG CTG         540
R   P   N   V   Y   W   I   N   K   T   D   N   S   L   L
                170                 175                 180
```

FIGURE 3A.2

```
GAC CAG GCT CTG CAG AAT GAC ACC GTC TTC TTG AAC ATG CGG GGC        585
D   Q   A   L   Q   N   D   T   V   F   L   N   M   R   G
                185                 190                 195

TTG TAT GAC GTG GTC AGC GTG CTG AGG ATC GCA CGG ACC CCC AGC        630
L   Y   D   V   V   S   V   L   R   I   A   R   T   P   S
                200                 205                 210

GTG AAC ATT GGC TGC TGC ATA GAG AAC GTG CTT CTG CAG CAG AAC        675
V   N   I   G   C   C   I   E   N   V   L   L   Q   Q   N
                215                 220                 225

CTG ACT GTC GGC AGC CAG ACA GGA AAT GAC ATC GGA GAG AGA GAC        720
L   T   V   G   S   Q   T   G   N   D   I   G   E   R   D
                230                 235                 240

AAG ATC ACA GAG AAT CCA GTC AGT ACC GGC GAG AAA AAC GCG GCC        765
K   I   T   E   N   P   V   S   T   G   E   K   N   A   A
                245                 250                 255

ACG TGG AGC ATC CTG GCT GTC CTG TGC CTG CTT GTG GTC GTG GCG        810
T   W   S   I   L   A   V   L   C   L   L   V   V   V   A
                260                 265                 270

GTG GCC ATA GGC TGG GTG TGC AGG GAC CGA TGC CTC CAA CAC AGC        855
V   A   I   G   W   V   C   R   D   R   C   L   Q   H   S
                275                 280                 285

TAT GCA GGT                                                       864
Y   A   G
        288
```

FIGURE 3B

```
hB7RP1      EKEVRAMVGS DVELSCACPE GSRFDLNDVY VYWQTSESKT VVTYHIPQNS   50
mB7RP1      ETEVGAMVGS NVVLSCIDPH RRHFNLSGLY VYWQIENPEV SVTYYLPYKS   50
Consensus   E.EV.AMVGS .V.LSC..P. ...F.L...Y VYWQ..... .VTY..P..S

hB7RP1      SLENVDSRYR NRALMSPAGM LRGDFSLRLF NVTPQDEQKF HCLVLSQ-SL   99
mB7RP1      PGINVDSSYK NRGHLSLDSM KQGNFSLYLK NVTPQDTQEF TCRVFMNTAT  100
Consensus   ...NVDS.Y. NR...S...M ..G.FSL.L. NVTPQD.Q.F .C.V......

hB7RP1      GFQEVLSVEV TLHVAANFSV PVVSAPHSPS Q-DELTFTCT SINGYPRPNV  148
mB7RP1      ELVKILEEVV RLRVAANFST PVISTSDSSN PGQERTYTCM SKNGYPEPNL  150
Consensus   .....L...V .L.VAANFS. PV.S...S.. ...E.T.TC. S.NGYP.PN.

hB7RP1      YWINKTDNSL LDQALQNDTV FLNMRGLYDV VSVLRIARTP SVNIGCCIEN  198
mB7RP1      YWINTTDNSL IDTALQNNTV YLNKLGLYDV ISTLRLPWTS RGDVLCCVEN  200
Consensus   YWIN.TDNSL .D.ALQN.TV .LN..GLYDV .S.LR...T. .....CC.EN

hB7RP1      VLLQQNLTVG SQTGNDIGER DKITENPVST GEKNAATWSI LAVLCLLVVV  248
mB7RP1      VALHQNITSI SQAESFTGNN TKNPQETHNN ELKVLV--PV LAVLAAAAFV  248
Consensus   V.L.QN.T.. SQ.....G.. .K........ ..K....... LAVL.....V

hB7RP1      AVAIGWVCRD RCLQHSYAG                                    267
mB7RP1      SFIIYR--RT R-PHRSYTGP KTVQLELTDH A                      276
Consensus   ...I....R. R....SY.G. .......... .
```

FIG. 4A

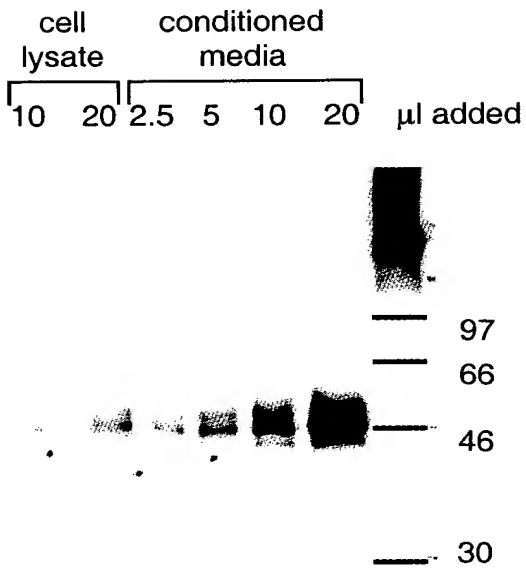


FIG. 4B

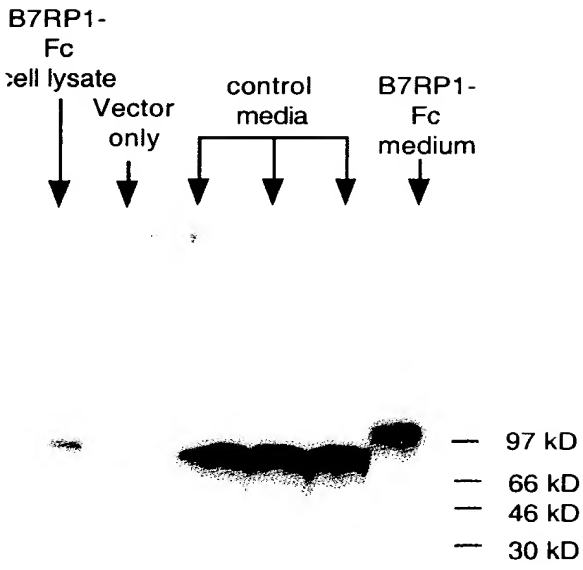


FIG. 5

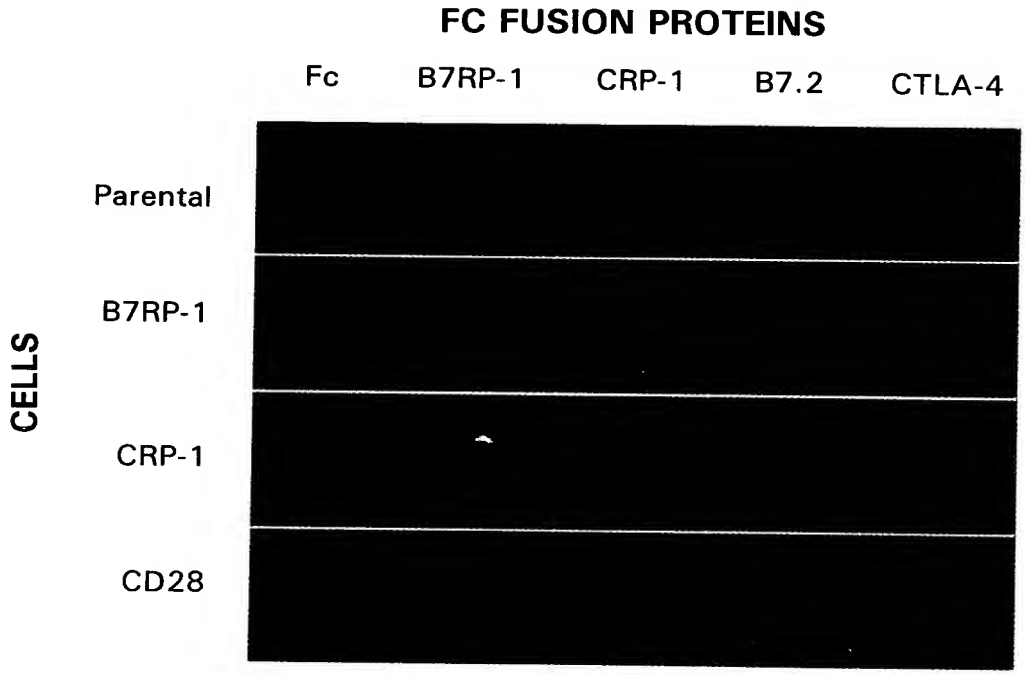


FIG. 6A

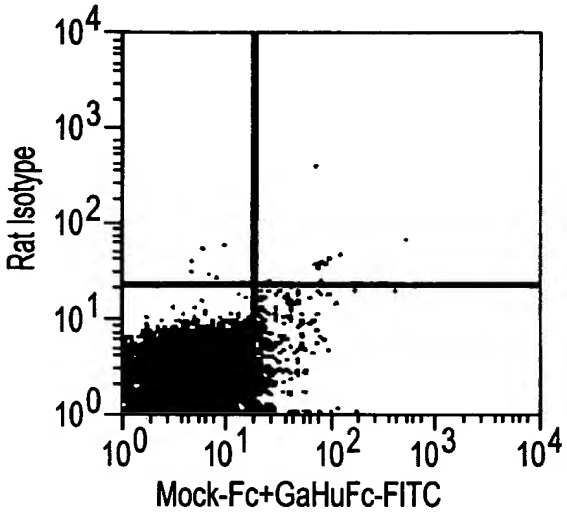


FIG. 6B

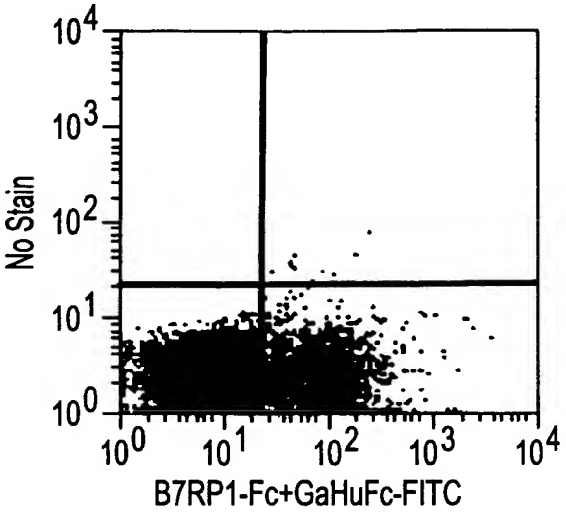


FIG. 6C

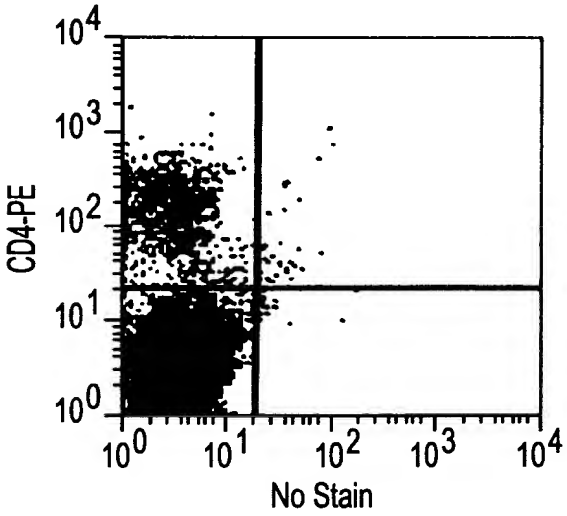


FIG. 6D

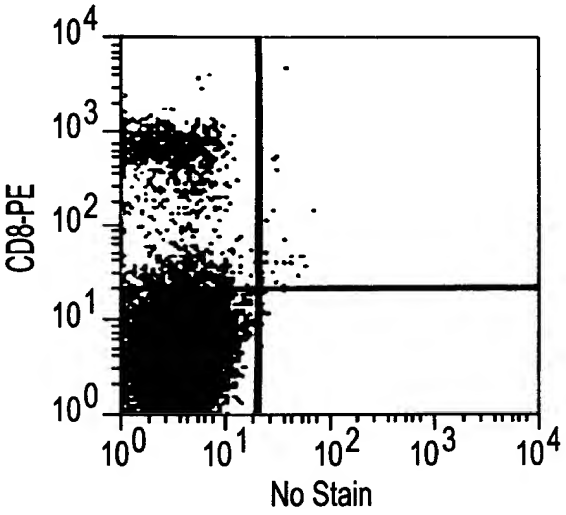


FIG. 6E

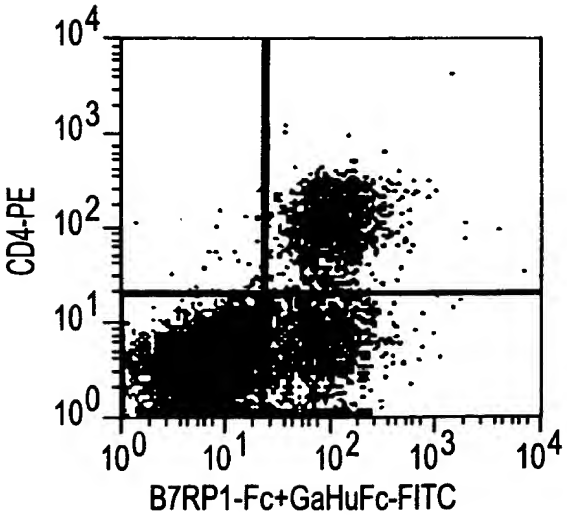


FIG. 6F

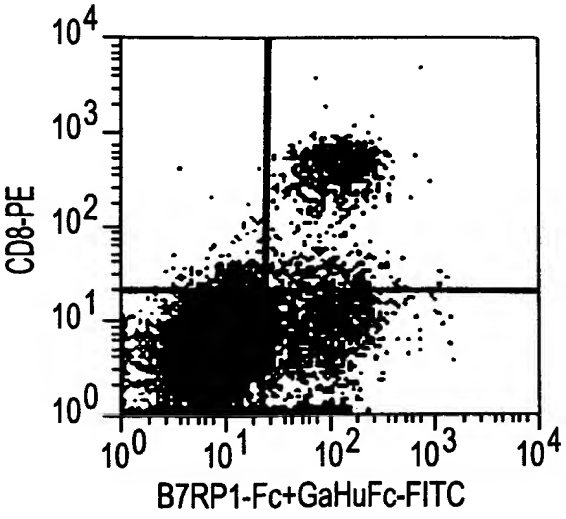


FIG. 7A

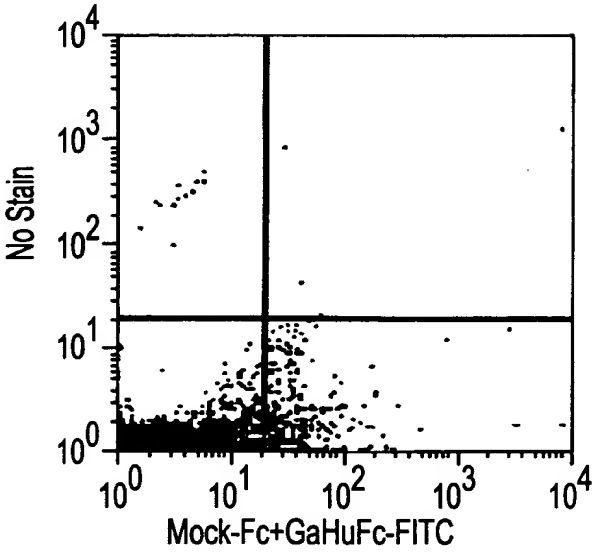


FIG. 7B

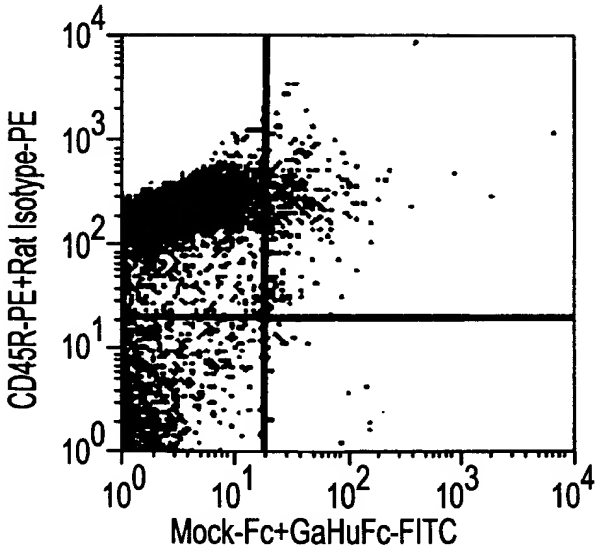


FIG. 7C

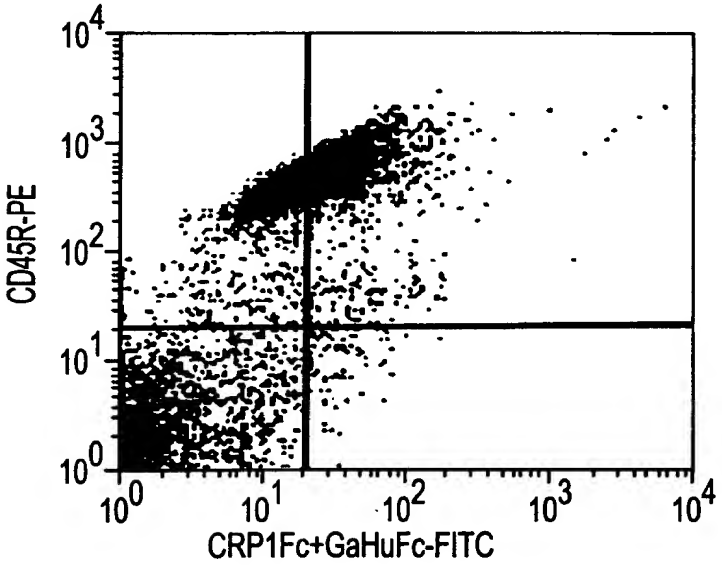


FIG. 8A

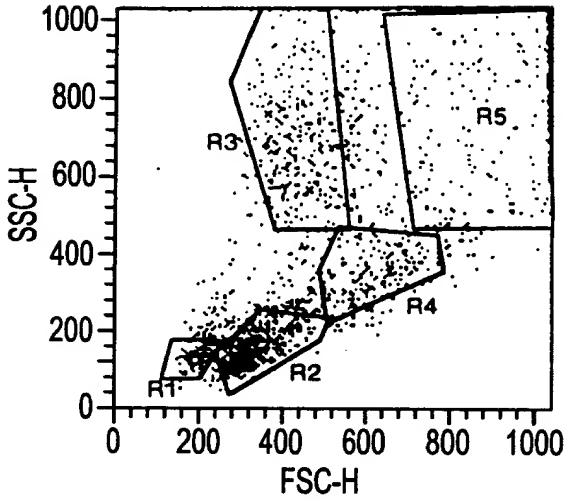


FIG. 8B

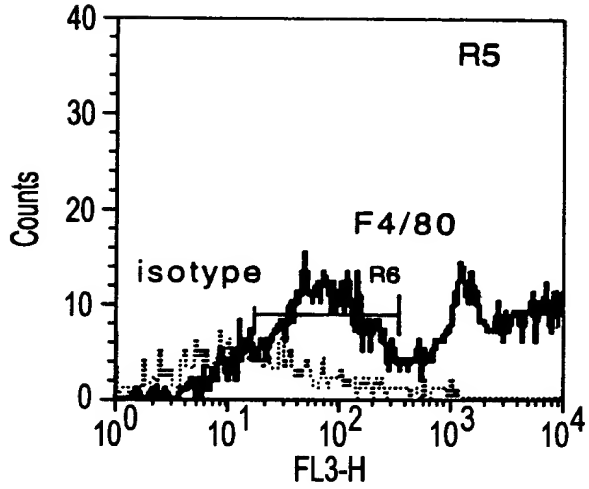


FIG. 8C

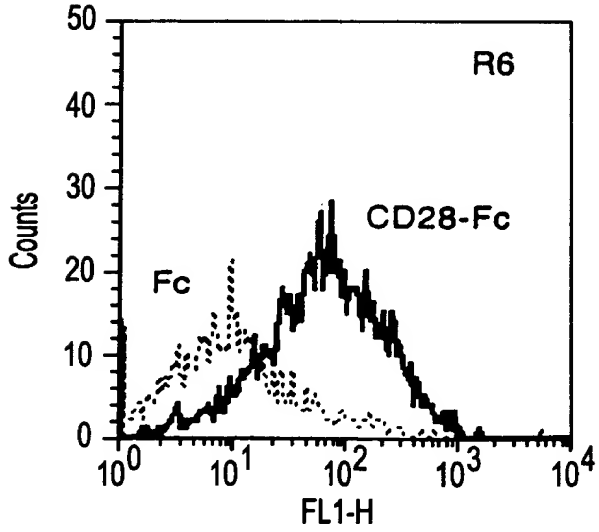


FIG. 9

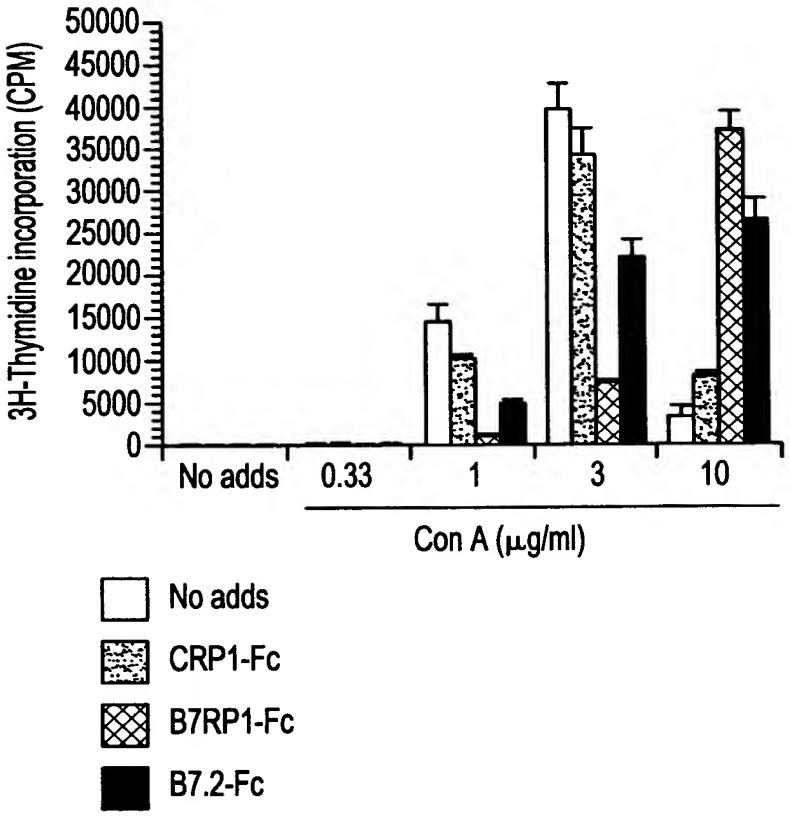


FIG. 10A

Lymph node-control#10

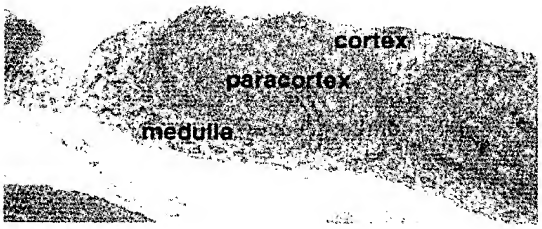


FIG. 10B

LN-WX11#40

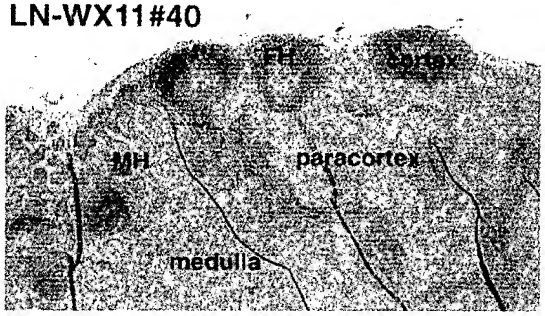


FIG. 10C

LN closeup-control#10

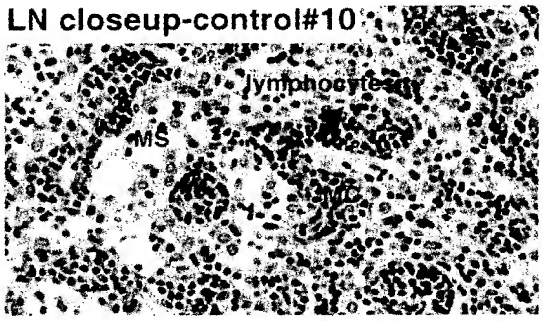


FIG. 10D

LN closeup-WX11#40

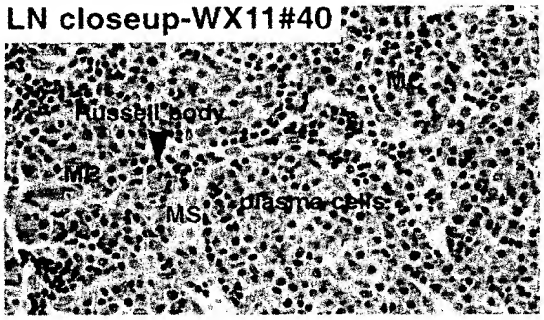


FIG. 10E

Spleen-control#10

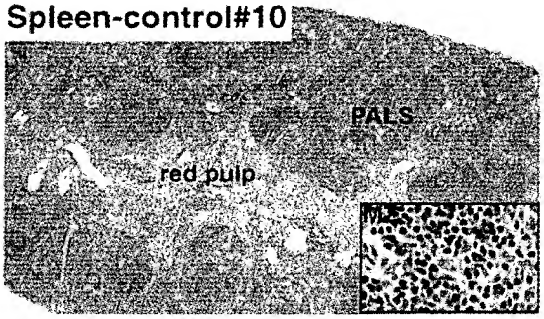


FIG. 10F

Spleen-WX11#6

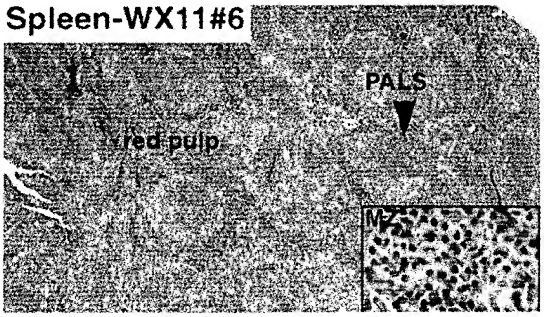


FIG. 10G

Ileum-control#25

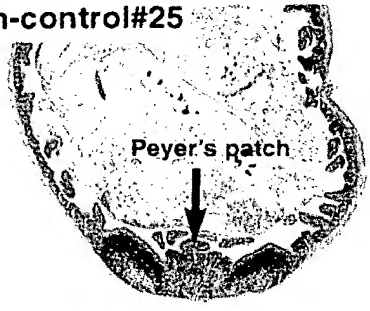


FIG. 10H

Ileum-WX11#32

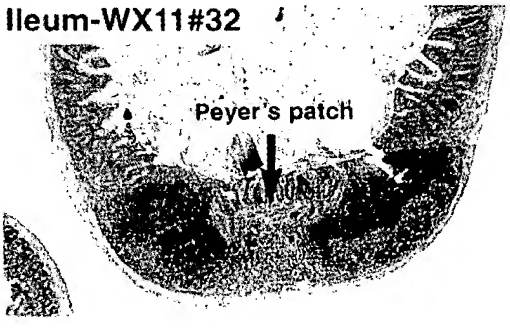
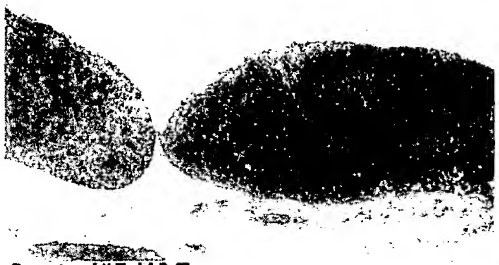


FIG. 11A



Control#5-H&E

FIG. 11B

WX11#33

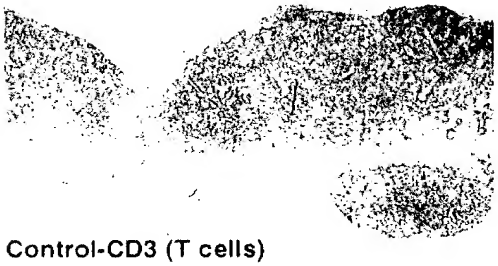
FIG. 11C

Control-B220 (B cells)

FIG. 11D

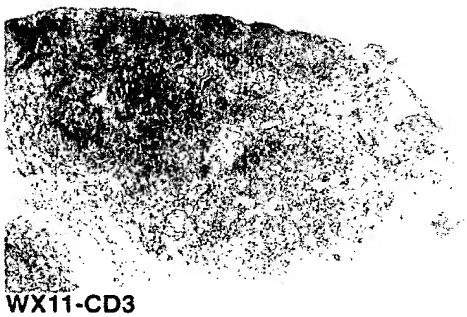
WX11-B220

FIG. 11E



Control-CD3 (T cells)

FIG. 11F



WX11-CD3

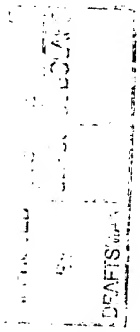
FIGURE 12A.1

```
GCTGGTACGCCTGCAGGTACCGGTCCGGAATTCCCGGGTCGACCCACGCGTCCGCCCACGCG   -138
TCCGCGGGAGCGCAGTTAGAGCCGATCTCCCGCGCCCCGAGGTTGCTCCTCTCCGAGGTCTC   -76
CCGCGGCCCAAGTTCTCCGCGCCCCGAGGTCTCCGCGCCCCGAGGTCTCCGCGGCCCGAGGT   -14
CTCCGCCCGCACC                                                     -1

ATG CGG CTG GGC AGT CCT GGA CTG CTC TTC CTG CTC TTC AGC AGC        45
M   R   L   G   S   P   G   L   L   F   L   L   F   S   S
                5                   10                  15

CTT CGA GCT GAT ACT CAG GAG AAG GAA GTC AGA GCG ATG GTA GGC        90
L   R   A  *D  *T  *Q  *E   K  *E   V   R   A  *M   V   G
                20                  25                  30

AGC GAC GTG GAG CTC AGC TGC GCT TGC CCT GAA GGA AGC CGT TTT       135
S   D   V   E   L   S   C   A   C   P   E   G   S   R   F
                35                  40                  45

GAT TTA AAT GAT GTT TAC GTA TAT TGG CAA ACC AGT GAG TCG AAA       180
D   L   N   D   V   Y   V   Y   W   Q   T   S   E   S   K
                50                  55                  60

ACC GTG GTG ACC TAC CAC ATC CCA CAG AAC AGC TCC TTG GAA AAC       225
T   V   V   T   Y   H   I   P   Q   N   S   S   L   E   N
                65                  70                  75

GTG GAC AGC CGC TAC CGG AAC CGA GCC CTG ATG TCA CCG GCC GGC       270
V   D   S   R   Y   R   N   R   A   L   M   S   P   A   G
                80                  85                  90

ATG CTG CGG GGC GAC TTC TCC CTG CGC TTG TTC AAC GTC ACC CCC       315
M   L   R   G   D   F   S   L   R   L   F   N   V   T   P
                95                  100                 105

CAG GAC GAG CAG AAG TTT CAC TGC CTG GTG TTG AGC CAA TCC CTG       360
Q   D   E   Q   K   F   H   C   L   V   L   S   Q   S   L
                110                 115                 120

GGA TTC CAG GAG GTT TTG AGC GTT GAG GTT ACA CTG CAT GTG GCA       405
G   F   Q   E   V   L   S   V   E   V   T   L   H   V   A
                125                 130                 135

GCA AAC TTC AGC GTG CCC GTC GTC AGC GCC CCC CAC AGC CCC TCC       450
A   N   F   S   V   P   V   V   S   A   P   H   S   P   S
                140                 145                 150

CAG GAT GAG CTC ACC TTC ACG TGT ACA TCC ATA AAC GGC TAC CCC       495
Q   D   E   L   T   F   T   C   T   S   I   N   G   Y   P
                155                 160                 165
```

FIGURE 12A.2

```
AGG CCC AAC GTG TAC TGG ATC AAT AAG ACG GAC AAC AGC CTG CTG          540
R   P   N   V   Y   W   I   N   K   T   D   N   S   L   L
                170                 175                 180

GAC CAG GCT CTG CAG AAT GAC ACC GTC TTC TTG AAC ATG CGG GGC          585
D   Q   A   L   Q   N   D   T   V   F   L   N   M   R   G
                185                 190                 195

TTG TAT GAC GTG GTC AGC GTG CTG AGG ATC GCA CGG ACC CCC AGC          630
L   Y   D   V   V   S   V   L   R   I   A   R   T   P   S
                200                 205                 210

GTG AAC ATT GGC TGC TGC ATA GAG AAC GTG CTT CTG CAG CAG AAC          675
V   N   I   G   C   C   I   E   N   V   L   L   Q   Q   N
                215                 220                 225

CTG ACT GTC GGC AGC CAG ACA GGA AAT GAC ATC GGA GAG AGA GAC          720
L   T   V   G   S   Q   T   G   N   D   I   G   E   R   D
                230                 235                 240

AAG ATC ACA GAG AAT CCA GTC AGT ACC GGC GAG AAA AAC GCG GCC          765
K   I   T   E   N   P   V   S   T   G   E   K   N   A   A
                245                 250                 255

ACG TGG AGC ATC CTG GCT GTC CTG TGC CTG CTT GTG GTC GTG GCG          810
T   W   S   I   L   A   V   L   C   L   L   V   V   V   A
                260                 265                 270

GTG GCC ATA GGC TGG GTG TGC AGG GAC CGA TGC CTC CAA CAC AGC          855
V   A   I   G   W   V   C   R   D   R   C   L   Q   H   S
                275                 280                 285

TAT GCA GGT GCC TGG GCT GTG AGT CCG GAG ACA GAG CTC ACT GGC          900
Y   A   G   A   W   A   V   S   P   E   T   E   L   T   G
                                                    300

CAC GTT TGA                                                         909
H   V   STOP
    302

CCGGAGCTCACCGCCCAGAGCGTGGACAGGGCTTCCGTGAGACGCCACCGTGAGAGGCCAGG     971
TGGCAGCTTGAGCATGGACTCCCAGACTGCAGGGGAGCACTTGGGGCAGCCCCCAGAAGGAC     1033
CACTGCTGGATCCCAGGGAGAACCTGCTGGCGTTGGCTGTGATCCTGGAATGAGGCCCTTTC     1095
```

FIGURE 12B



```
human       MRLGSP---- ---------- ---------G L-LF-LLFSS LRADTQEKEV   25
mouse       MQLKCPCFVS LGTRQPVWKK LHVSSGFFSG LGLFLLLLSS LCAASAETEV   50
Consensus   M.L..P.... .......... .........G L.LF.LL.SS L.A...E.EV   50

human       RAMVGSDVEL SCACPEGSRF DLNDVYVYWQ TSESKTVVTY HIPQNSSLEN   75
mouse       GAMVGSNVVL SCIDPHRRHF NLSGLYVYWQ IENPEVSVTY YLPYKSPGIN  100
Consensus   .AMVGS.V.L SC..P....F .L...YVYWQ .......VTY ..P..S...N  100

human       VDSRYRNRAL MSPAGMLRGD FSLRLFNVTP QDEQKFHCLV LSQ-SLGFQE  124
mouse       VDSSYKNRGH LSLDSMKQGN FSLYLKNVTP QDTQEFTCRV FMNTATELVK  150
Consensus   VDS.Y.NR.. .S...M..G. FSL.L.NVTP QD.Q.F.C.V ..........  150

human       VLSVEVTLHV AANFSVPVVS APHSPSQ-DE LTFTCTSING YPRPNVYWIN  173
mouse       ILEEVVRLRV AANFSTPVIS TSDSSNPGQE RTYTCMSKNG YPEPNLYWIN  200
Consensus   .L...V.L.V AANFS.PV.S ...S.....E .T.TC.S.NG YP.PN.YWIN  200

human       KTDNSLLDQA LQNDTVFLNM RGLYDVVSVL RIARTPSVNI GCCIENVLLQ  223
mouse       TTDNSLIDTA LQNNTVYLNK LGLYDVISTL RLPWTSRGDV LCCVENVALH  250
Consensus   .TDNSL.D.A LQN.TV.LN. .GLYDV.S.L R...T..... .CC.ENV.L.  250

human       QNLTVGSQTG NDIGERDKIT ENPVSTGEKN AATWSILAVL CLLVVVAVAI  273
mouse       QNITSISQAE SFTGNNTKNP QETHNNELKV LV--PVLAVL AAAAFVSFII  298
Consensus   QN.T..SQ.. ...G...K.. ........K. ......LAVL .....V...I  300

human       GWVCRDRCLQ HSYAGAWAVS PETELTGHV                         302
mouse       YR--RTR-PH RSYTGPKTVQ LE--LTDHA                         322
Consensus   ....R.R... .SY.G...V. .E..LT.H.                         329
```

FIGURE 13A.1

```
AACAATTTCACACAGGAAACAGCTATGACCATGATTACGCCAAGCTCTAATACGA                -111
CTCACTATAGGGAAAGCTGGTACGCCTGCAGGTACCGGTCCGGAATTCCCGGGTC               -56
GACCCACGCGTCCGTGAACACTGAACGCGAGGACTGTTAACTGTTTCTGGCAAAC                -1

ATG AAG TCA GGC CTC TGG TAT TTC TTT CTC TTC TGC TTG CGC ATT             45
M   K   S   G   L   W   Y   F   F   L   F   C   L   R   I
                5                   10                  15

AAA GTT TTA ACA GGA GAA ATC AAT GGT TCT GCC AAT TAT GAG ATG             90
K   V   L   T  *G  *E   I   N   G   S   A   N   Y   E   M
                20                  25                  30

TTT ATA TTT CAC AAC GGA GGT GTA CAA ATT TTA TGC AAA TAT CCT            135
F   I   F   H   N   G   G   V   Q   I   L   C   K   Y   P
                35                  40                  45

GAC ATT GTC CAG CAA TTT AAA ATG CAG TTG CTG AAA GGG GGG CAA            180
D   I   V   Q   Q   F   K   M   Q   L   L   K   G   G   Q
                50                  55                  60

ATA CTC TGC GAT CTC ACT AAG ACA AAA GGA AGT GGA AAC ACA GTG            225
I   L   C   D   L   T   K   T   K   G   S   G   N   T   V
                65                  70                  75

TCC ATT AAG AGT CTG AAA TTC TGC CAT TCT CAG TTA TCC AAC AAC            270
S   I   K   S   L   K   F   C   H   S   Q   L   S   N   N
                80                  85                  90

AGT GTC TCT TTT TTT CTA TAC AAC TTG GAC CAT TCT CAT GCC AAC            315
S   V   S   F   F   L   Y   N   L   D   H   S   H   A   N
                95                  100                 105

TAT TAC TTC TGC AAC CTA TCA ATT TTT GAT CCT CCT CCT TTT AAA            360
Y   Y   F   C   N   L   S   I   F   D   P   P   P   F   K
                110                 115                 120

GTA ACT CTT ACA GGA GGA TAT TTG CAT ATT TAT GAA TCA CAA CTT            405
V   T   L   T   G   G   Y   L   H   I   Y   E   S   Q   L
                125                 130                 135

TGT TGC CAG CTG AAG TTC TGG TTA CCC ATA GGA TGT GCA GCC TTT            450
C   C   Q   L   K   F   W   L   P   I   G   C   A   A   F
                140                 145                 150

GTT GTA GTC TGC ATT TTG GGA TGC ATA CTT ATT TGT TGG CTT ACA            495
V   V   V   C   I   L   G   C   I   L   I   C   W   L   T
                155                 160                 165
```

FIGURE 13A.2

```
AAA AAG AAG TAT TCA TCC AGT GTG CAC GAC CCT AAC GGT GAA TAC          540
K   K   K   Y   S   S   S   V   H   D   P   N   G   E   Y
                170                 175                 180

ATG TTC ATG AGA GCA GTG AAC ACA GCC AAA AAA TCT AGA CTC ACA          585
M   F   M   R   A   V   N   T   A   K   K   S   R   L   T
                185                 190                 195

GAT GTG ACC CTA TAA                                                  600
D   V   T   L   STOP
                199

TATGGAACTCTGGCACCCAGGCATGAAGCACGTTGGCCAGTTTTCCTCAACTTGA              655
AGTGCAAGATTCTCTTATTTCCGGGACCACGGAGAGTCTGACTTAACTACATACA              710
TCTTCTGCTGGTGTTTTGTTCAATCTGGAAGAATGACTGTATCAGTCAATGGGGA              765
TTTTAACAGACTGCCTTGGTACTGCCGAGTCCTCTCAAAACAAACACCCTCTTGC              820
AACCAGCTTTGGAGAAAGCCCAGCTCCTGTGTGCTCACTGGGAGTGGAATCCCTG              875
TCTCCACATCTGCTCCTAGCAGTGCATCAGCCAGTAAAACAAACACATTTACAAG              930
AAAAATGTTTTAAAGATGCCAGGGGTACTGAATCTGCAAAGCAAATGAGCAGCCA              985
AGGACCAGCATCTGTCCGCATTTCACTATCATACTACCTCTTCTTTCTGTAGGGA             1040
TGAGAATTCCTCTTTTAATCAGTCAAGGGAGATGCTTCAAAGCTGGAGCTATTTT             1095
ATTTCTGAGATGTTGATGTGAACTGTACATTAGTACATACTCAGTACTCTCCTTC             1150
AATTGCTGAACCCCAGTTGACCATTTTACCAAGACTTTAGATGCTTTCTTGTGCC             1205
```

FIGURE 13B

```
hCRP1    MKSGLWYFFLFCLRIKVLTGEINGSANYEMFIFHNGGVQILCKYPDIVQQ   50
mCRP1    MKPYFCRVFVFCFLIRLLTGEINGSADHRMFSFHNGGVQISCKYPETVQQ   50

hCRP1    FKMQLLKGGQILCDLTKTKGSGNTVSIKSLKFCHSQLSNNSVSFFLYNLD   100
mCRP1    LKMRLFREREVLCELTKTKGSGNAVSIKNPMLCLYHLSNNSVSFFLNNPD   100

hCRP1    HSHANYYFCNLSIFDPPPFKV.TLTGGYLHIYESQLCCQLKFWLPIGCAA   149
mCRP1    SSQGSYYFCSLSIFDPPPFQERNLSGGYLHIYESQLCCQLKLWLPVGCAA   150

hCRP1    FVVVCILGCILICWLTKKKYSSSVHDPNGEYMFMRAVNTAKKSRLTDVTL   199
mCRP1    FVVVLLFGCILIIWFSKKKYGSSVHDPNSEYMFMAAVNTNKKSRLAGVTS   200
```

FIG. 14A

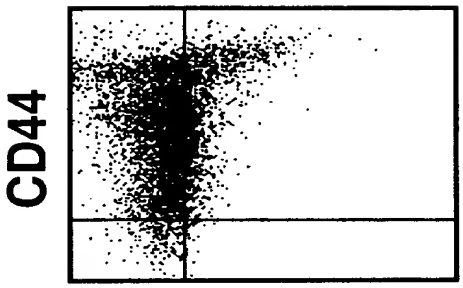


FIG. 14B

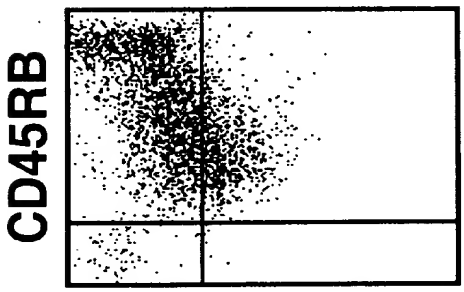


FIG. 14C

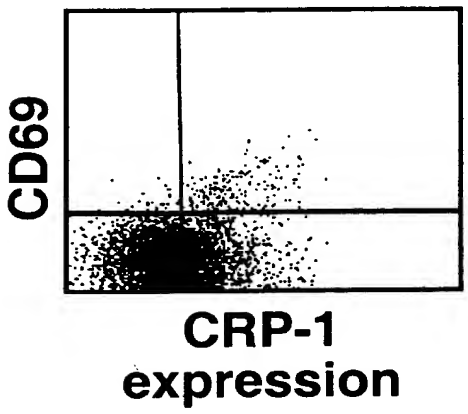


FIG. 15A

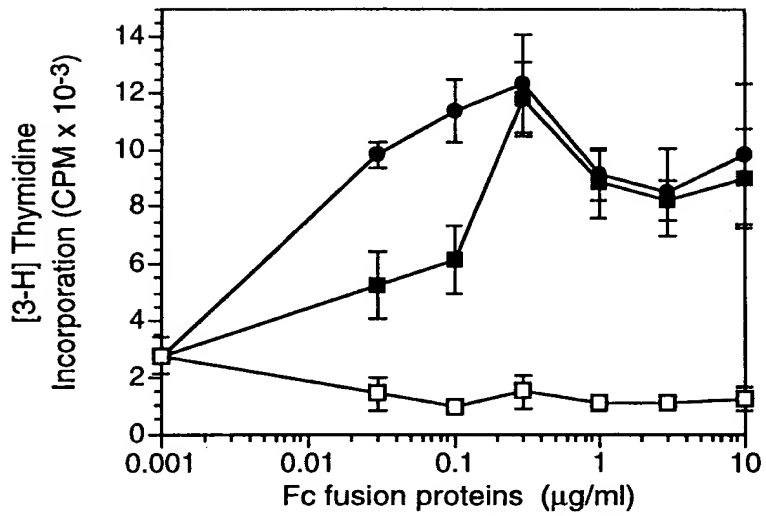


FIG. 15B

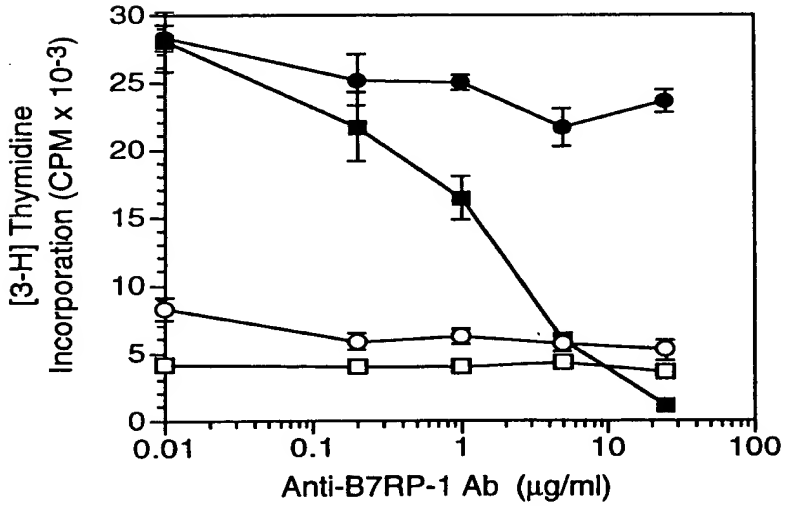


FIG. 16A

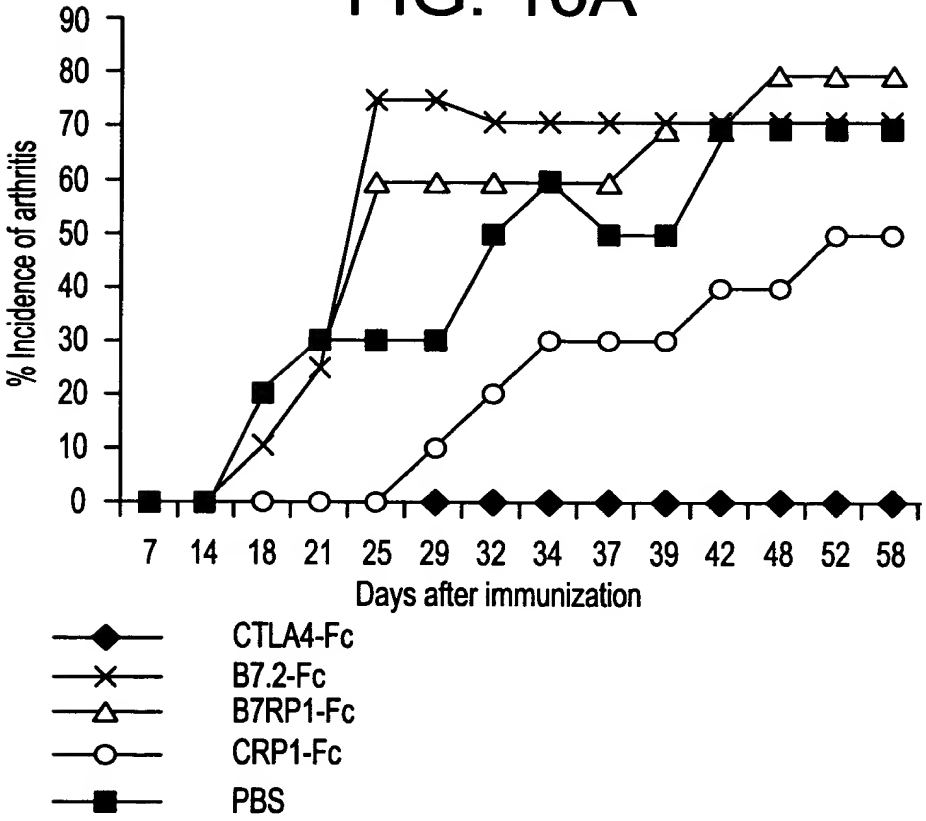


FIG. 16B

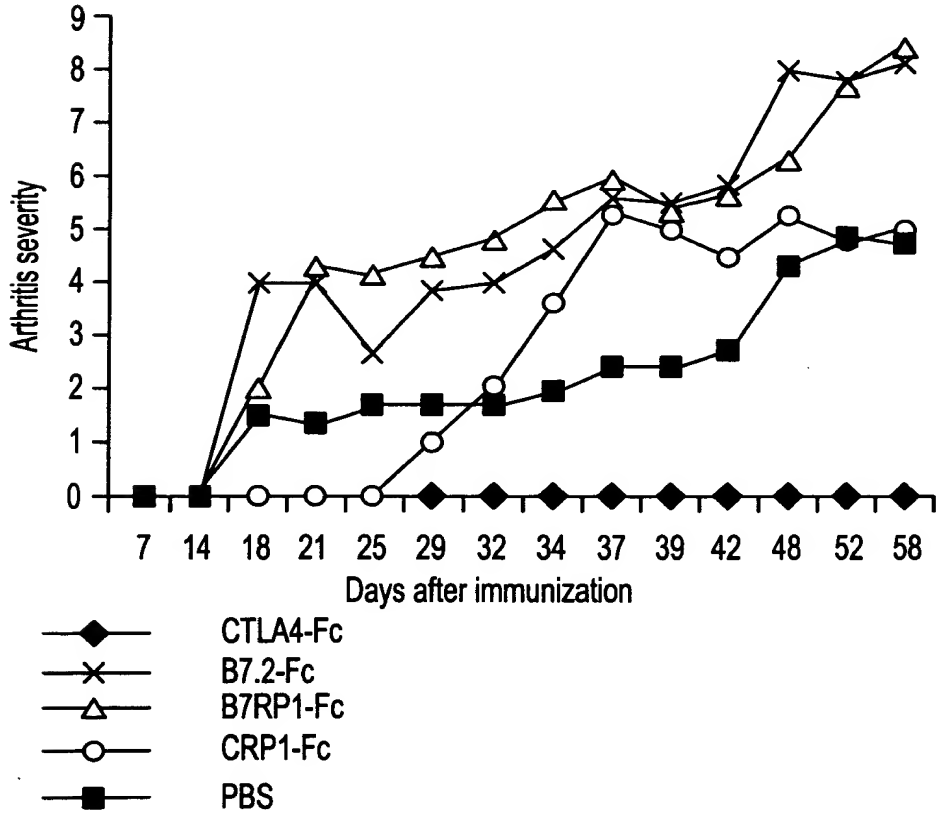
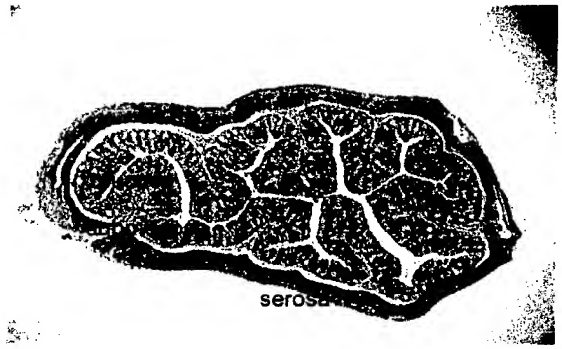
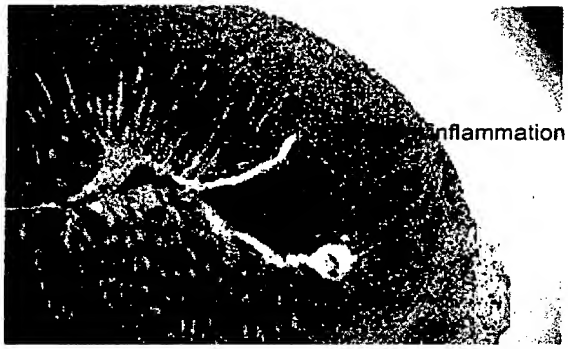


FIG. 17A



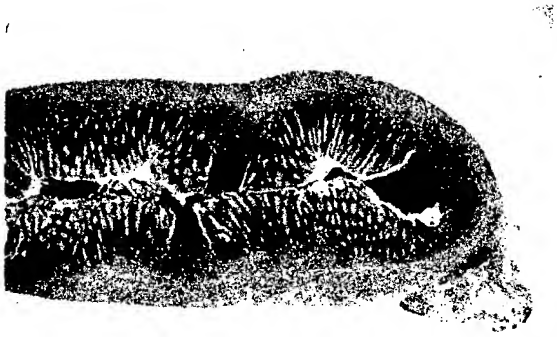
Control mouse#53F: Prox. colon 40X

FIG. 17B



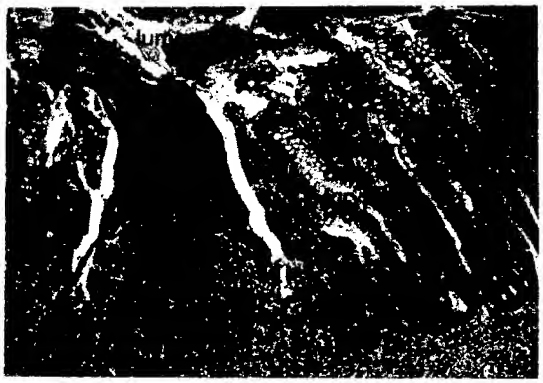
Mouse#111F: Prox. colon 40X

FIG. 17C



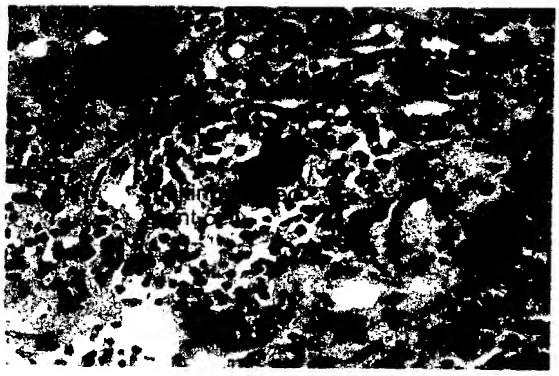
Mouse#111F: Prox. colon 20X

FIG. 17D



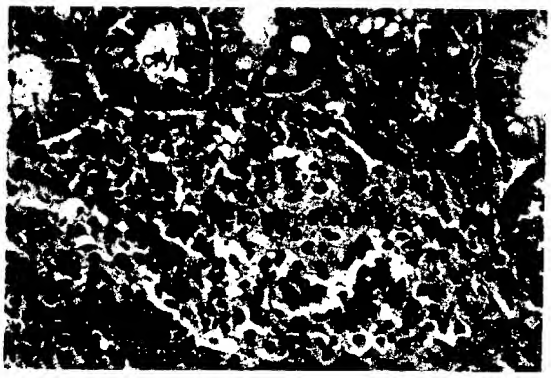
Mouse#111F: closeup of mucosa 100X

FIG. 17E



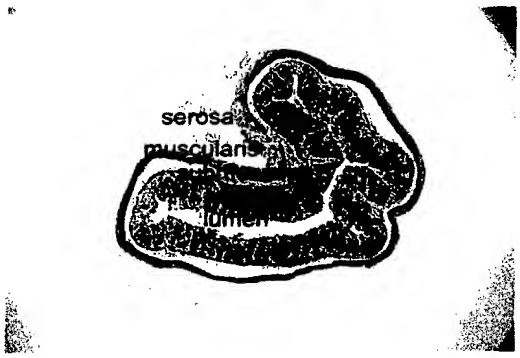
Mouse#112F: Giant cell, submucosa

FIG. 17F



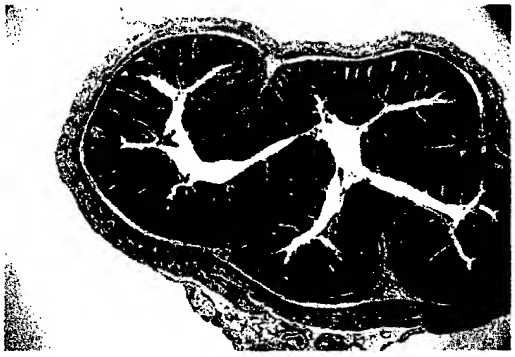
Mouse#112F: epithelioid macrophages

FIG. 18A



Control mouse#53F: Distal colon, 40X

FIG. 18B

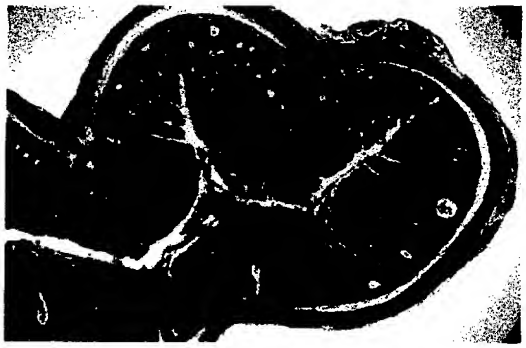


Mouse#111F: Distal colitis, 40X

FIG. 18C

Mouse#55M: Distal colitis, 40X

FIG. 18D

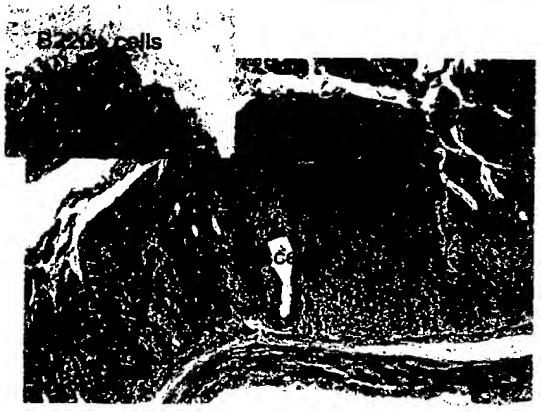


Mouse#112F: Distal colon, 40X

FIG. 18E

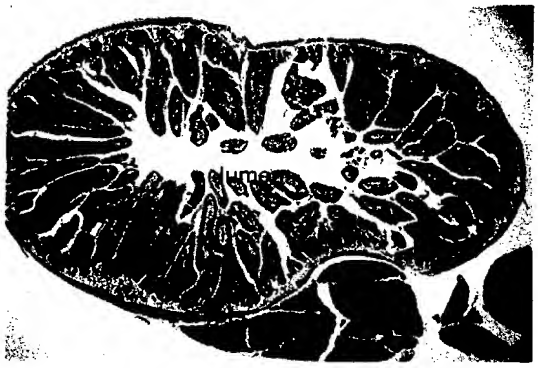
Mouse#112: CD3+ T-cells, 40X

FIG. 18F



Mouse#112: closeup, 100X

FIG. 19A

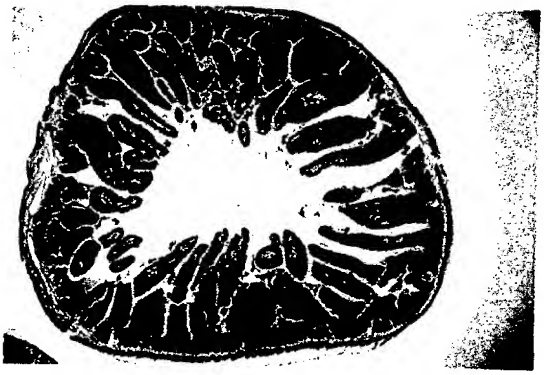


Control mouse#53F: duodenum, 40X

FIG. 19B

Mouse#51F: duodenum, 40X

FIG. 19C

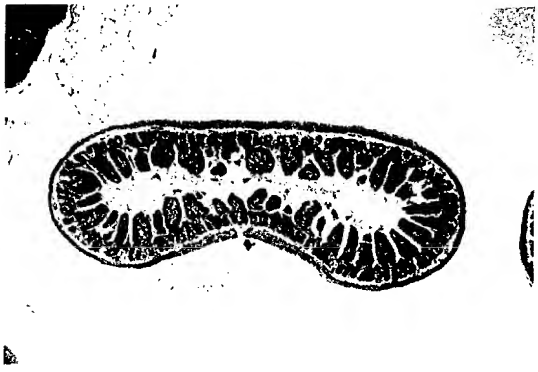


Control mouse#53F: jejunum, 40X

FIG. 19D

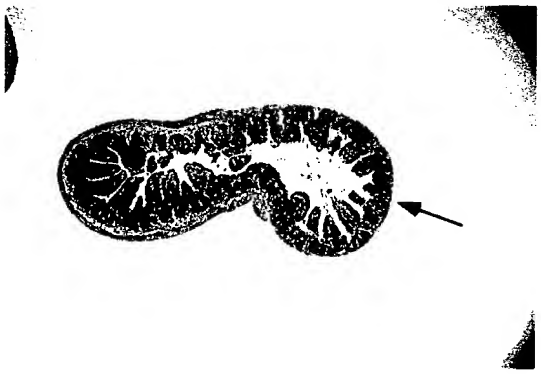
Mouse#51F: jejunal hyperplasia, 40X

FIG. 19E



Mouse#53F: ileum, 40X

FIG. 19F



Mouse#231M: ileal atrophy, 40X

FIG. 20

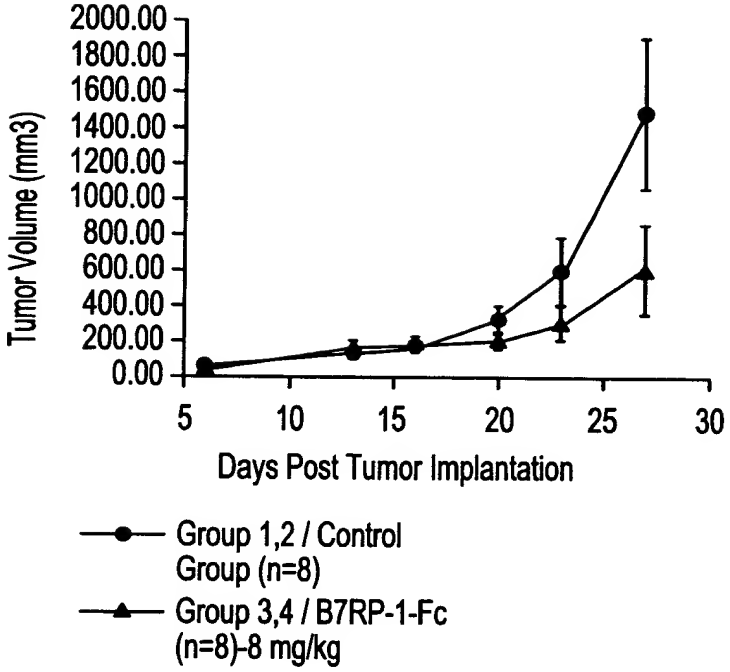


FIG. 21A

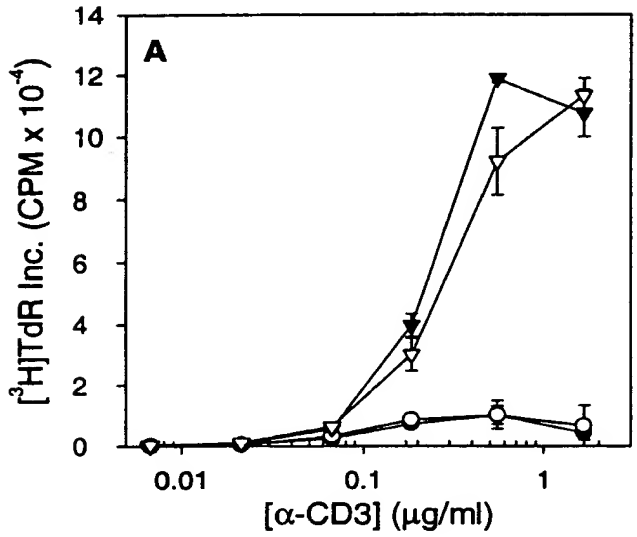


FIG. 21B

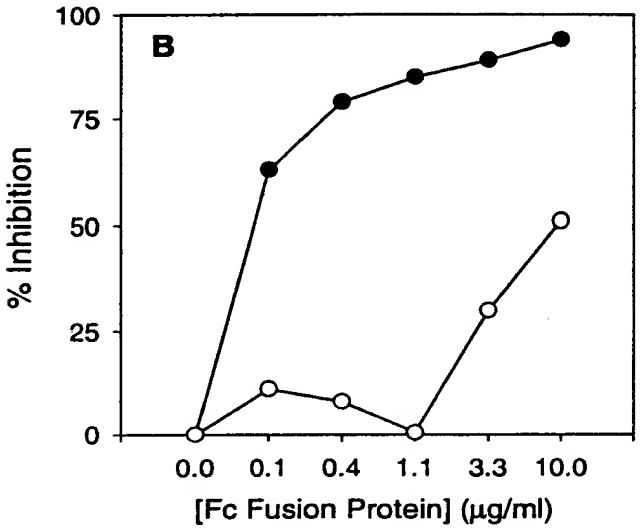


FIG. 21C

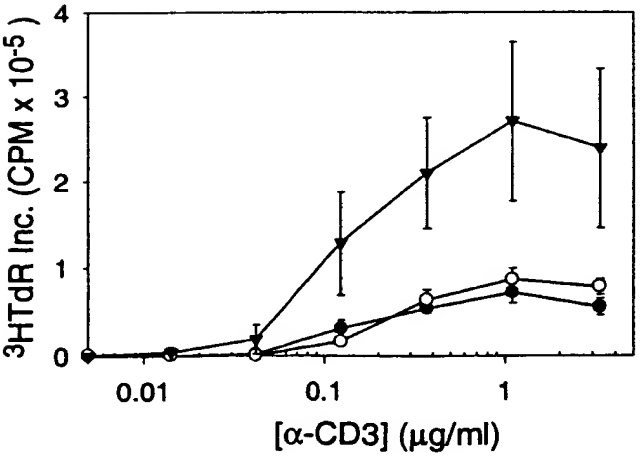


FIG. 21D

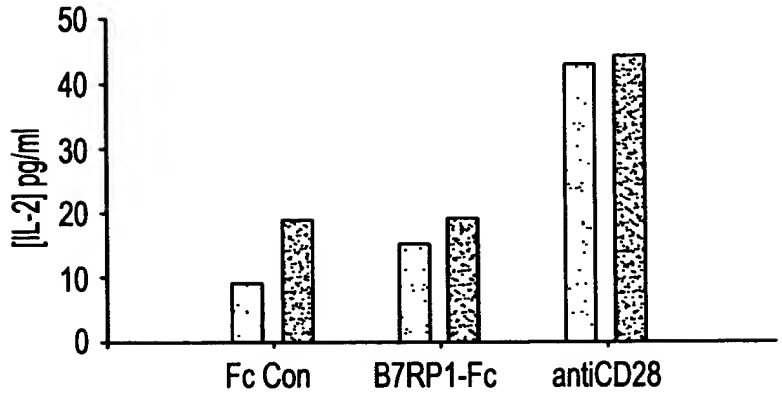


FIG. 21E

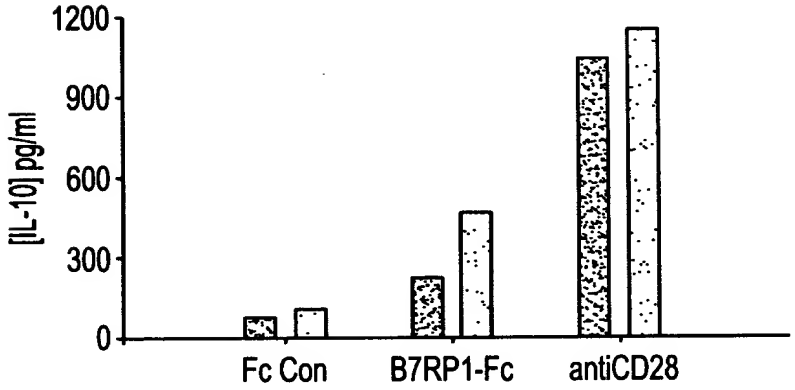


FIG. 21F

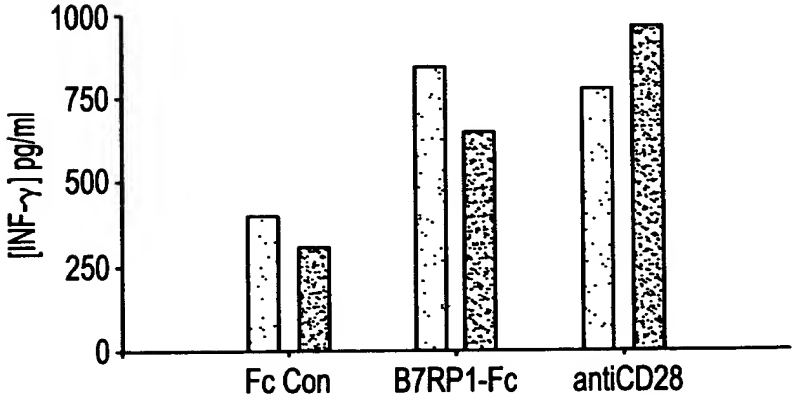


FIG. 22

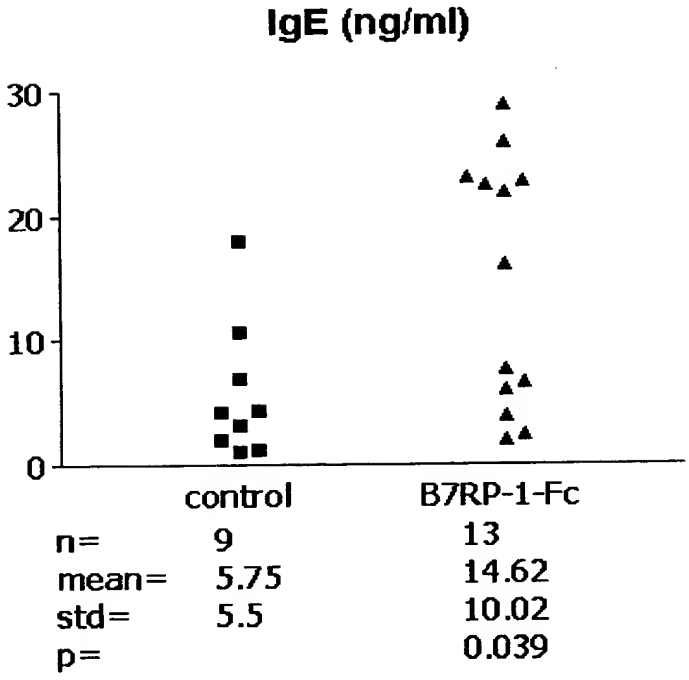


FIG. 23